

HYPOTHESES & PREDICTION

Hypothesis: Bats, rodents, and primates are affected more by segmented viruses compared to other mammalian orders. The segmentation of these viruses promotes mutation and reassortment, increasing the likelihood of cross-species transmission and enhancing their zoonotic potential.

Prediction: Bats, rodents, and primates will have a higher percentage of segmented viruses than the other mammalian orders, and this will be reflected by the vSegmentedTF column. Since genome segmentation allows more mutation and reassortment, cross-species transmission will occur frequently and result in a greater likelihood of zoonotic diseases from these orders. In contrast, other mammalian orders that are not as affected by segmented viruses will exhibit less frequent cross-species transmission and fewer zoonotic disease occurrences.

HOW DATA WAS COLLECTED

The data we will use for this analysis are from the Clover database:

Mammal_viruses-Associations and the HP3 virus dataset. Clover is a comprehensive database that merges other datasets about viruses and their mammal hosts. Clover has also been edited to keep the data's taxonomy consistent with NCBI. We will focus on segmented viruses, particularly those that can spread between species (the zoonotic viruses).

For the Mammal_Viruse_Associations dataset, includes information on which viruses infect which mammals. We will be using HostOrder to separate mammalian groups such as bats, rodents, and primates.

For the HP3 virus dataset, it includes more detailed information about each virus. In this case, the vSegmentedTF column is our key focus. Because we will be looking at the segmentation to determine whether it will have a stronger effect on certain host orders than another. We will also make sure that virus names in the vVirusNameCorrected column are consistent to avoid mismatch during the analysis.

CITATION

R Gibb, GF Albery, DJ Becker, L Brierley, R Connor, TA Dallas, EA Eskew, MJ Farrell, AL Rasmussen, SJ Ryan, AR Sweeny, CJ Carlson, T Poisot. Data proliferation, reconciliation, and synthesis in viral ecology. First posted January 16, 2021. bioRxiv DOI: 10.1101/2021.01.14.426572.